MBE Author-Subject Index: Volume 10

A-monomer, 552

ABSHER, R., 282

acanthocephalan, 660

Acipenser transmontanus, 326

actin: 689; gene, 205

actinomycete, 1303

adaptation: molecular, 457

ADEY, NILS B., 552

Agrobacterium, 437

alanine:glyoxylate aminotransferase 1, 704

alcohol dehydrogenase, 362, 605, 1215

algae: green, 1317

alignment(s): local, 73; multiple, 73;

sequence, 1170

ALVAREZ, G., 823

AMEMIYA, CHRIS T., 60

Americans: Native, 23

anchovy, 319

ANDERSON, CORT L., 605

angiosperms, 140

ANXOLABÉHÈRE, DOMINIQUE, 791

Apis mellifera, 488

ÁRNASON, ÚLFUR, 306, 960

ASHLEY, M. V., 282

Astyanax faxciatus, 527

ATCHLEY, WILLIAM R., 1150

Australia, 484

Aves, 1196

AVISE, JOHN C., 342

AYALA, FRANCISCO JOSÉ, 1030

AZEN, EDWIN A., 497

BACHMANN, LUTZ, 647

BAKER, ROBERT J., 944

BARKER, J. S. F., 484

BECKENBACH, ANDREW T., 326, 619

BENEDICT, CATHERINE M., 769

BERNARDI, GIORGIO, 186

BERNATCHEZ, LOUIS, 1002

BHATTACHARYA, DEBASHISH, 689 BIANCHI, NESTOR O., 271

BIGOT, YVES, 383

BONHOMME, FRANÇOIS, 719

branch lengths: least-squares estimates,

1073

bride of sevenless, 1030

BRINKMANN, HENNER, 140

BRITTEN, ROY J., 205, 1370

Brown, James R., 326

BURKE, WILLIAM D., 163

BURNETT, JEAN, 635

Ca++, 221

cadherin, 539

Caledia captiva, 855

CAMPESAN, SUSANNA, 127

CAREW, ELIZABETH A., 605

CERFF, RÜDIGER, 140

Cetacea, 306, 960

cGMP and cAMP channels, 221

chaetognath, 660

CHAKRABORTY, RANAJIT, 1112

CHANDY, K. GEORGE, 221

CHANG, BELINDA, 1115

channels: cGMP and cAMP, 221; ion, 221

chaperones, 103, 1343

character analysis, 707

charr: brook, 1002

Chelonia mydas, 342

CHEMNICK, LEONA G., 571

chimpanzees, 512

Chlamydiae, 892, 1327

chromosome: sex, 271

cichlids, 1015, 1060

CLARK, ANDREW G., 769, 1096

classification, 1170

coalescence: 2; time, 23

COATS, STEPHEN R., 732

codon: bias, 605, 1239; optimization, 397;

synonymous, 397

coevolution, 892

complement, 48

composition: base, 437; third-base G+C,

205

congruence: 944; taxonomic, 1170

conservation: estimation, 488

CORREDOR, VLADIMIR, 924

Corvidae, 1196

COSTA, RODOLFO, 127

costs: gap, 707

COURNOYER, BENOIT, 1303

CRACRAFT, JOEL, 1196

Crassostrea virginica, 342

crossing-over: unequal, 1041

crystallin: α , 103

cyanobacteria, 704

cytochrome-b, 488, 751, 873, 1196

cytochrome oxidase II, 619, 1115

D-loop, 326

DANPURE, CHRISTOPHER J., 704

DANZMANN, ROY G., 1002

DE LA MAZA, LUIS, M., 892 DE ZOYSA, PRIYAL A., 704

DENELL, ROB, 1041

difference: pairwise, 23

DILLON, MARY C., 296

disequilibrium: gametic, 823

distance: correction, 471; matrix, 221, 471

distribution: Γ, 1396

divergence: patterns, 719; times, 1030 diversity, 60

diversity, oo

diversity-enhancing selection, 1048

DIXON, MICHAEL T., 256

DJIAN, P., 1136

DNA: chloroplast, 414; evolution, 647; fingerprint, 571; mitochondrial, 2, 23, 271, 282, 319, 326, 375, 484, 619; mobile,

163; repetitive, 127, 383, 552, 647; satellite, 306; sequences, 497, 552, 842, 1327;

SSU-ribosomal, 1317

DOWNIE, STEPHEN R., 414

drift: molecular, 1030

Drosophila: 127, 362, 769, 791, 823, 842,

1030, 1041; buzzatii, 484; Hawaiian, 362; hydei, 397; melanogaster, 397; montium subgroup, 375; obscura, 647;

pseudoobscura, 619; virilis, 635; willistoni, 605

duplication(s): 48; exon, 1041

EASLEY, K., 1136

Ectodini, 751

EDGELL, MARSHALL H., 552, 719

EERNISSE, DOUGLAS J., 1170

EICKBUSH, DANNA G., 163

EICKBUSH, THOMAS H., 163

Emiliania huxlevi, 689

ENEA, VINCENZO, 924

EPSTEIN, LLOYD M., 732

Escherichia coli, 1380

estimation: unbiased, 677, 1073

evidence: total, 170

evolution(ary): 60, 383, 457, 539, 689, 971, 1259; accelerated, 497; actin gene, 205;

adaptive, 243; chlamydia, 892; colicin, 1048, 1380; distance, 677; hominoid,

1115; human, 512, 927, 1115;

molecular, 282, 449, 619, 660, 769,

1115, 1380; rate(s), 243, 271, 892, 1215;

salamander, 732; simulated, 471

exon duplication, 1041 eye lens, 103

fibronectin type III, 539

FIGUEROA, FELIPE, 48

FITCH, DAVID H. A., 397

FITCH, WALTER M., 713, 892, 1150

FORKMANN, GERT, 140

fossils, 1170

founder effect, 484

Fox, James G., 1327

Frankia sp., 1303

FRIEDMAN, THOMAS B., 635

fungi: higher, 431

GARCÍA-ARENAL, FERNANDO, 449

gene(s): 60; cloning, 1327; conversion, 271,

971; deletions, 414; diversity, 1112; du-

plications, 497, 635; flow, 342, 590; β -globin, 73; histone, 397; intron/exon,

605; involucrin, 1136; nuclear, 1360;

rearrangement, 60

genome: 457; composition, 186; evolution, 647

GEYER, CHARLES J., 571

globin(s): α-gene(s), 73

glyceraldehyde-3-phosphate

dehydrogenase, 140

GOUY, MANOLO, 1303

GRAHAM, TERESA A., 732

GREEN, BARBARA, 732 GREEN, H., 1136

GRÉTARSDÓTTIR, S., 306

GULLBERG, ANETTE, 960

GUTMAN, GEORGE, 221

Gymnogyps californianus, 571

gymnosperms, 140

HAIRE, ROBERT N., 60

HALLIBURTON, RICHARD, 484

HAMILTON, MEREDITH J., 944

HAMMER, MICHAEL F., 971

hamster proliferative ileitis, 1327

HANZAWA, NAOTO, 590

HARDISON, Ross, 73

HARRY, DAVID E., 1215

HARTL, DANIEL L., 1030

HAYASHI, SEIJI, 23

HBV, 457

heat-shock protein: 243, 1343; HSP70,

243; small, 103

HELM-BYCHOWSKI, KATHLEEN, 1196

hemoglobin, 73 heterochromatin, 791 heteroplasmy, 319 heterozygosity, 1112 HEY, JODY, 804, 1239 HIGGINS, DESMOND G., 914 Hill-Robertson effect, 1239 HILLIS, DAVID M., 256 HINDS-FREY, KRISTIN R., 60 histatins, 497 hitchhiking, 842, 1239 Ho, Yu, 1327 HOELZER, G. A., 282 HOLLAND, P. W. H., 660 hominoid evolution, 1115 HONEYCUTT, RODNEY, L., 590 HORAI, SATOSHI, 23 HOWELL, NEIL, 488 HUANG, E., 1136 HUGHES, AUSTIN, L., 243, 1343, 1360 HUGHES, MARIANNE K., 1360 HULST, MICHELE, 60 human: evolution, 927; mtDNA variation, 1115; populations, 927 HUNT, JOHN A., 362 HUTCHISON, CLYDE A., III, 552, 719 hybridization; interspecific, 1289 hydrogenase, 704 hypothesis: multiregional, 1115

immunoglobulin, 60, 539
inheritance: biparental, 319
internal transcribed spacers (ITS), 1273
intron/exon evolution, 605
intron(s): group I, 1317
inversions, 414
involucrin genes, 1136
ion channels, 221
isolates, 590
IWABE, NAOYUKI, 539

JACQUES, MICHELINE, 791 JAKUBCZAK, JOHN, 163 JIN, LI, 1112

K⁺, 221 Karl, Stephen A., 342 karyotype, 855 Klein, Dagmar, 48 Klein, Jan, 48, 1060 Kliman, Richard M., 804, 1239 Kluge, Arnold G., 1170 Knox, Eric B., 414 Kondo, Rumi, 23 Kornfield, Irv, 1015 Kozak, Keith A., 1227 Kreitman, Martin, 1259 Kuma, Kei-ichi, 539 Kyriacou, Charalambos P., 127

LAI, CHING-LUNG, 457 LANIGAN, CAROLINE M. S., 1096 LAU, JOHNSON YN, 457 LAUDER, IAN J., 457 LEHMANN, MONIQUE, 791 LEICHT, BRENDA G., 769 lepidoptera, 1259 LEUNISSEN, JACK A. M., 103 likelihood: 221; maximum, 1396 LIN, HSIANG-JU, 457 LIN, JENNY, 1115 lineage sorting, 1015 LINEs: 163; -1, 719 linkage group, 1227 LITMAN, GARY W., 60 LITMAN, RONDA T., 60 LIU. HONG, 619 Lobelia, 414 loci: anonymous nuclear, 342 LOOTENS, SUSAN, 635 loss parsimony, 1150 LYCKEGAARD, EVA M. S., 769 LYDIATE, DEREK, 140 L1 repetitive DNA, 552

McCutchan, Thomas F., 914 MCENTIRE, BRENDA, 1227 MCKECHNIE, STEPHEN W., 1259 MAGOULAS, ANTONIOS, 319 major histocompatibility complex, 48, major outer-membrane protein (MOMP), 1327 malaria, 914 mammals, 73, 873 MARCHANT, ADAM D., 855 MARÍN, ANTONIO, 437 MARTIN, ANDREW P., 873 MARTIN, WILLIAM, 140 MARTÍNEZ-ZAPATER, JOSÉ M., 437 mauritiana, 804 maximum likelihood, 1395 MAYER, WERNER E., 48 MELNICK, DON J., 282 method(s): Jukes and Cantor's, 677: Kimura's, 677; Tajima and Nei's, 677

MEYER, AXEL, 751

Mhc. 2

mice: 719; inbred, 1150

MILLER, WEBB, 73

Mimulus, 1273

minimum misplaced quartets, 471

minisatellites: hypervariable, 1112

mitochondria(1): 1259; D-Loop, 296; DNA control region, 512; DNA diversity, 590, 855, 944, 960, 1002, 1015, 1196, 1289; human variation, 1115

MIYATA, TAKASHI, 539

mole-rats, 590

molecular: adaptation, 457; drift, 1030; evolution, 769, 1115; phylogeny, 140, 944, 1303; population genetics, 842;

systematics, 140, 362, 944, 1303

MONTCHAMP-MOREAU, CATHERINE, 791 MORAN, PAUL, 1015

MORIZOT, DONALD C., 1227

morphology, 1170

mouse (mice): 552, 1136; house, 971; pneumonitis, 892, 1327

MOYA, ANDRÉS, 449

Muller's ratchet, 1239

multigene family, 221, 243

multiregional: theory, 927; hypothesis, 1115

multiple alignments, 73

mutation: advantageous, 842; bias, 186, 437; rate, 205

Mycobacterium: leprae, 1343; tuberculosis,

myosin alkali light chain, 769

Na+, 221

NAIRN, RODNEY S., 1227

NAKAGAWA-HATTORI, YUKO, 23

NEI, MASATOSHI, 1, 512, 927, 1073

neighbor joining, 221, 471

NELSON, KIMBERLYN, 590

NEVO, EVIATAR, 590

nif D, 1303

NISHIDA, HIROMI, 431

nitrogenase, 1303

nucleotide: differences, 677; divergence, 1096; diversity, 1096; sequence, 23, 1227; substitutions, 271, 512

NORMAND, PHILIPPE, 1303

number of nucleotide differences, 677

OHUigin, COLM, 48, 1060 OLIVER, JOSÉ L., 437

OLSEN, JEANINE L., 1317

ONO, HIDEKI, 1060

organization: segmental, 60

OTA, TATSUYA, 497

outer-membrane proteins, 892

PABÓN-PEÑA, LIL M., 732

PALMER, JEFFREY D., 414

PALUMBI, STEPHEN R., 873

PAMILO, PEKKA, 271

PAN, DEBORAH, 1115

Paradisaeidae, 1196

paralogy, 1360

parsimony: 221, 971, 1150, 1196; weighted, 221

PCR-RFLP, 1289

PEACH, SHARON E., 732

PEIXOTO, ALEXANDRE A., 127

period gene, 127

period locus, 804

PERIOUET, GEORGES, 383

PETERSON, ELLENA M., 892

PHILLIPS, M., 1136

phylogenetic tree, 23, 471, 552, 927, 1327 phylogeny: 221, 256, 375, 414, 527, 689,

914, 1150, 1170, 1215, 1273; inference, 1396; macaque, 282; molecular, 306,

431, 605 PIERCE, NAOMI, 1259

PISSIOS, PAVLOS, 375

Plasmodium, 914, 924

polymerase chain reaction (PCR), 342,

660, 751, 1096

polymorphism: 48, 804, 1030, 1112; RFLP, 342; transspecies, 2

population genetics: 326, 1112, 1239;

structure, 2

POWELL, JEFFREY R., 605

primates, 48

promoter: snRNA, 732

protein(s): 1170; outer membrane, 892;

ribosomal S6, 1002, 1041, 1227; stress, 1343; yolk, 804

pseudogene, 971

Ptilonorhynchidae, 1196

RAPDs, 1096

radiation: adaptive, 751, 1060

RAST, JONATHAN, 60

rat, 1136

rate(s): substitution, 1360

recombination, 1239

region(s): conserved, 488; control 751, 960, 1002, 1259; locus control, 73

relatedness, 571

relative-rate test, 140

repeats: shared, 1136

restriction-fragment-length polymorphism (RFLP); 342, 1002, 1227

restriction map variation, 823

restriction site: 414; enzymes, 484; maps, 282, 375

retrotransposable elements, 163

retransposon, 791, 1370

reverse transcriptase, 1370

rhythms: biological, 127

ribosomal protein S6, 1041

ribozyme, 732

ribulose-1, 5-biphosphatecarboxylase/ oxygenase, 140

RICE, R. H., 1136

RILEY, MARGARET A., 1048, 1380

RITLAND, CAROL E., 1273

RITLAND, KERMIT, 1273

RNA: fingerprinting, 449; ribosomal, 163, 256, 431, 660, 924, 1170; self-cleaving, 732

RNase H, 1370

RODRÍGUEZ-CEREZO, EMILIO, 449

ROESS, WILLIAM, 60

ROJAS-ROUSSE, DANIÈLE, 383

ROLIG, RHONDA L., 1227

RONSSERAY, STÉPHANE, 791

ROYCHOUDHURY, ARUN K., 927

rRNA: 18S, 914

RUVOLO, MARYELLEN, 1115

RYDER, OLIVER A., 571

RZHETSKY, ANDRE, 1073

SABATINI, LINDA M., 497

SAEDLER, HEINZ, 140

Saitoella complicata, 431 salamander evolution, 732

satellite, 2, 732

Scaptodrosophila, 362

Scaptomyza, 362

SCHICHMAN, STEVEN A., 552

SCHÖNIGER, MICHAEL, 471

SCHWENK, KLAUS, 1289

SCOURAS, ZACHARIAS G., 375

Scrophulariaceae, 1273

sechellia, 804

selection: 186, 1380; balancing; 2; periodic,

449

selective gene expression constraints, 437

sequence: alignment, 1170; blocks,

conserved, 296; variation, 1273 1731: 791

SHAMBLOTT, MICHAEL J., 60

sharks, 873

SHAW, DAVID D., 855

SILVER, LEE M., 971

SIMON, M., 1136

simulans, 804

SIU, TAK-SHING, 457

SMITH, MICHAEL J., 326

SMITH, TEMPLE F., 1327

SOGIN, MITCHELL L., 689

SONODA, SHUNRO, 23

Spalax ehrenbergi, 590

speciation, 590, 804, 1060

species flocks, 751 1015

SPERLICH, DIETHER, 647

splicing: alternative pre-mRNA, 769

SPRINGER, MARK S., 1370

STAM, WYTZE T., 1317

STARMER, WILLIAM T., 527

statherin, 497

statistical power, 823

Stenodermatini, 944

STEPHAN, WOLFGANG, 842

STEWART, MARY J., 1041

STICKEL, SHAWN K., 689

STILLS, HAROLD F., JR., 1327

STRAUS, NEIL A., 1273

STRAUSBAUGH, LINDA D., 397

Streptomyces albus, 1343

STRONG, MICHAEL, 221

structure: secondary, 256

STURMBAUER, CHRISTIAN, 751

superfamily, 539

substitutions: rare synonymous, 205;

synonymous and nonsynonymous, 1048

SUGIYANA, JUNTA, 431

symbiosis, 1303

synteny, 1227

systematics, 707

T-cell epitopes, 1343

T-DNA, 437

t haplotype, 971

TAJIMA, FUMIO, 677

TAJIMA, KAZUO, 23

TAKAHATA, NAOYUKI, 2

TAMURA, KOICHIRO, 497

Taphrina wiesneri, 431

TAYLOR, MARTIN F. J., 1259

TELFORD, MAXIMILIAN J., 660

1410 VOLUME INDEX

theory: multiregional, 927; neutral, 449; out-of-Africa, 927 THOMAS, RICHARD H., 362 THOMPSON, ELIZABETH A., 571 TICHY, HERBERT, 1060 transition/transversion: bias, 512; ratio, 707 transposable elements, 719 triangle inequality, 707 tyrosine kinase, 539

urate oxidase (UO), 635 uricase, 635 Urospora, 1317

Vaccine, 892
VAN DEN BUSSCHE, RONALD A., 944
VAN OPPEN, MADELEINE J. H., 1317
VANLERBERGHE, FLAVIE, 719
variability, 457
variation: geographic, 855; spatial rate, 1396
vision: color, 527
voles, 719
VON DORNUM, MIRANDA, 1115
von Haeseler, Arnot, 471
VOORTER, CHRISTINA E. M., 103

WALTER, RONALD B., 1227 wasp: parasitoid, 383 WATERS, ANDREW P., 914 WEI, YUE WANG, 619
weighting differences, 471
whales: beaked, 306; sperm, 296, 306, 960;
whalebone, 960
WHEELER, WARD C., 707
WHITTAM, THOMAS S., 1
WICHMAN, HOLLY A., 944
WIDEGREN, BENGT, 960
WIEHE, THOMAS H. E., 842
WRIGHT, JONATHAN M., 296

Xenopus laevis, 1360 XIONG, YUE, 163

Y chromosome, 1150 Yang, Ziheng, 1396 Yokoyama, Ruth, 527 Yokoyama, Shozo, 527, 1215 Yonekawa, Hiromichi, 590

Zapata, C., 823 Zehr, Sarah, 1115 zesie, 804 Zíx, 271 Zíy, 271 Zhang, Li, 1327 Zhang, You-Xun, 1327 Zilch, Anna, 60 Zouros, Eleftherios, 319

